

SEQUENCE LISTING

<110> HIHARA, SATOSHI
DOI, HIROFUMI

<120> INTERACTION INHIBITORS, METHOD OF DETECTING INTERACTION
INHIBITOR AND KIT FOR DETECTING INTERACTION INHIBITOR

<130> 028567-0145

<140> 10/568,578

<141> 2006-02-17

<150> PCT/JP2004/011686

<151> 2004-08-13

<150> JP 2003-295204

<151> 2003-08-19

<160> 11

<170> PatentIn Ver. 3.3

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 1

atgtcgccat ttcttcggat tgg

23

<210> 2

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 2

tcaggatatc agccgctcc

19

<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 3
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<210> 4
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 4
tcaaagctgg aaaccttcc 19

<210> 5
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 5
gcggccgcaa tggcagaaga tgatccatat ttggg 35

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
primer

<400> 6
ctcgagttac atggttccat gcttcatccc 30

<210> 7
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 7
gcggccgcaa tggacgaact gttccccctc 30

<210> 8
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 8
 ctcgagtttag gagctgatct gactcagc

28

<210> 9
 <211> 706
 <212> PRT
 <213> Homo sapiens

<400> 9
 Met Ser Pro Phe Leu Arg Ile Gly Leu Ser Asn Phe Asp Cys Gly Ser
 1 5 10 15
 Cys Gln Ser Cys Gln Gly Glu Ala Val Asn Pro Tyr Cys Ala Val Leu
 20 25 30
 Val Lys Glu Tyr Val Glu Ser Glu Asn Gly Gln Met Tyr Ile Gln Lys
 35 40 45
 Lys Pro Thr Met Tyr Pro Pro Trp Asp Ser Thr Phe Asp Ala His Ile
 50 55 60
 Asn Lys Gly Arg Val Met Gln Ile Ile Val Lys Gly Lys Asn Val Asp
 65 70 75 80
 Leu Ile Ser Glu Thr Thr Val Glu Leu Tyr Ser Leu Ala Glu Arg Cys
 85 90 95
 Arg Lys Asn Asn Gly Lys Thr Glu Ile Trp Leu Glu Leu Lys Pro Gln
 100 105 110
 Gly Arg Met Leu Met Asn Ala Arg Tyr Phe Leu Glu Met Ser Asp Thr
 115 120 125
 Lys Asp Met Asn Glu Phe Glu Thr Glu Gly Phe Phe Ala Leu His Gln
 130 135 140
 Arg Arg Gly Glu Ile Lys Gln Ala Lys Val His His Val Lys Cys His
 145 150 155 160
 Glu Phe Thr Ala Thr Phe Phe Pro Gln Pro Thr Phe Cys Ser Val Cys
 165 170 175
 His Glu Phe Val Trp Gly Leu Asn Lys Gln Gly Tyr Gln Cys Arg Gln
 180 185 190
 Cys Asn Ala Ala Ile His Lys Lys Cys Ile Asp Lys Val Ile Ala Lys
 195 200 205

Cys Thr Gly Ser Ala Ile Asn Ser Arg Glu Thr Met Phe His Lys Glu
 210 215 220
 Arg Phe Lys Ile Asp Met Pro His Arg Phe Lys Val Tyr Asn Tyr Lys
 225 230 235 240
 Ser Pro Thr Phe Cys Glu His Cys Gly Thr Leu Leu Trp Gly Leu Ala
 245 250 255
 Arg Gln Gly Leu Lys Cys Asp Ala Cys Gly Met Asn Val His His Arg
 260 265 270
 Cys Gln Thr Lys Val Ala Asn Leu Cys Gly Ile Asn Gln Lys Leu Met
 275 280 285
 Ala Glu Ala Leu Ala Met Ile Glu Ser Thr Gln Gln Ala Arg Cys Leu
 290 295 300
 Arg Asp Thr Glu Gln Ile Phe Arg Glu Gly Pro Val Glu Ile Gly Leu
 305 310 315 320
 Pro Cys Ser Ile Lys Asn Glu Ala Arg Pro Pro Cys Leu Pro Thr Pro
 325 330 335
 Gly Lys Arg Glu Pro Gln Gly Ile Ser Trp Glu Ser Pro Leu Asp Glu
 340 345 350
 Val Asp Lys Met Cys His Leu Pro Glu Pro Glu Leu Asn Lys Glu Arg
 355 360 365
 Pro Ser Leu Gln Ile Lys Leu Lys Ile Glu Asp Phe Ile Leu His Lys
 370 375 380
 Met Leu Gly Lys Gly Ser Phe Gly Lys Val Phe Leu Ala Glu Phe Lys
 385 390 395 400
 Lys Thr Asn Gln Phe Phe Ala Ile Lys Ala Leu Lys Lys Asp Val Val
 405 410 415
 Leu Met Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val Leu
 420 425 430
 Ser Leu Ala Trp Glu His Pro Phe Leu Thr His Met Phe Cys Thr Phe
 435 440 445
 Gln Thr Lys Glu Asn Leu Phe Phe Val Met Glu Tyr Leu Asn Gly Gly
 450 455 460
 Asp Leu Met Tyr His Ile Gln Ser Cys His Lys Phe Asp Leu Ser Arg
 465 470 475 480
 Ala Thr Phe Tyr Ala Ala Glu Ile Ile Leu Gly Leu Gln Phe Leu His
 485 490 495
 Ser Lys Gly Ile Val Tyr Arg Asp Leu Lys Leu Asp Asn Ile Leu Leu
 500 505 510

Asp Lys Asp Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys Glu
 515 520 525
 Asn Met Leu Gly Asp Ala Lys Thr Asn Thr Phe Cys Gly Thr Pro Asp
 530 535 540
 Tyr Ile Ala Pro Glu Ile Leu Leu Gly Gln Lys Tyr Asn His Ser Val
 545 550 555 560
 Asp Trp Trp Ser Phe Gly Val Leu Leu Tyr Glu Met Leu Ile Gly Gln
 565 570 575
 Ser Pro Phe His Gly Gln Asp Glu Glu Glu Leu Phe His Ser Ile Arg
 580 585 590
 Met Asp Asn Pro Phe Tyr Pro Arg Trp Leu Glu Lys Glu Ala Lys Asp
 595 600 605
 Leu Leu Val Lys Leu Phe Val Arg Glu Pro Glu Lys Arg Leu Gly Val
 610 615 620
 Arg Gly Asp Ile Arg Gln His Pro Leu Phe Arg Glu Ile Asn Trp Glu
 625 630 635 640
 Glu Leu Glu Arg Lys Glu Ile Asp Pro Pro Phe Arg Pro Lys Val Lys
 645 650 655
 Ser Pro Phe Asp Cys Ser Asn Phe Asp Lys Glu Phe Leu Asn Glu Lys
 660 665 670
 Pro Arg Leu Ser Phe Ala Asp Arg Ala Leu Ile Asn Ser Met Asp Gln
 675 680 685
 Asn Met Phe Arg Asn Phe Ser Phe Met Asn Pro Gly Met Glu Arg Leu
 690 695 700
 Ile Ser
 705

<210> 10
 <211> 706
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Ser Pro Phe Leu Arg Ile Gly Leu Ser Asn Phe Asp Cys Gly Ser
 1 5 10 15
 Cys Gln Ser Cys Gln Gly Glu Ala Val Asn Pro Tyr Cys Ala Val Leu
 20 25 30
 Val Lys Glu Tyr Val Glu Ser Glu Asn Gly Gln Met Tyr Ile Gln Lys
 35 40 45
 Lys Pro Thr Met Tyr Pro Pro Trp Asp Ser Thr Phe Asp Ala His Ile
 50 55 60

Asn	Lys	Gly	Arg	Val	Met	Gln	Ile	Ile	Val	Lys	Gly	Lys	Asn	Val	Asp	65	70	75	80
Leu	Ile	Ser	Glu	Thr	Thr	Val	Glu	Leu	Tyr	Ser	Leu	Ala	Glu	Arg	Cys	85	90	95	
Arg	Lys	Asn	Asn	Gly	Lys	Thr	Glu	Ile	Trp	Leu	Glu	Leu	Lys	Pro	Gln	100	105	110	
Gly	Arg	Met	Leu	Met	Asn	Ala	Arg	Tyr	Phe	Leu	Glu	Met	Ser	Asp	Thr	115	120	125	
Lys	Asp	Met	Asn	Glu	Phe	Glu	Thr	Glu	Gly	Phe	Phe	Ala	Leu	His	Gln	130	135	140	
Arg	Arg	Gly	Ala	Ile	Lys	Gln	Ala	Lys	Val	His	His	Val	Lys	Cys	His	145	150	155	160
Glu	Phe	Thr	Ala	Thr	Phe	Phe	Pro	Gln	Pro	Thr	Phe	Cys	Ser	Val	Cys	165	170	175	
His	Glu	Phe	Val	Trp	Gly	Leu	Asn	Lys	Gln	Gly	Tyr	Gln	Cys	Arg	Gln	180	185	190	
Cys	Asn	Ala	Ala	Ile	His	Lys	Lys	Cys	Ile	Asp	Lys	Val	Ile	Ala	Lys	195	200	205	
Cys	Thr	Gly	Ser	Ala	Ile	Asn	Ser	Arg	Glu	Thr	Met	Phe	His	Lys	Glu	210	215	220	
Arg	Phe	Lys	Ile	Asp	Met	Pro	His	Arg	Phe	Lys	Val	Tyr	Asn	Tyr	Lys	225	230	235	240
Ser	Pro	Thr	Phe	Cys	Glu	His	Cys	Gly	Thr	Leu	Leu	Trp	Gly	Leu	Ala	245	250	255	
Arg	Gln	Gly	Leu	Lys	Cys	Asp	Ala	Cys	Gly	Met	Asn	Val	His	His	Arg	260	265	270	
Cys	Gln	Thr	Lys	Val	Ala	Asn	Leu	Cys	Gly	Ile	Asn	Gln	Lys	Leu	Met	275	280	285	
Ala	Glu	Ala	Leu	Ala	Met	Ile	Glu	Ser	Thr	Gln	Gln	Ala	Arg	Cys	Leu	290	295	300	
Arg	Asp	Thr	Glu	Gln	Ile	Phe	Arg	Glu	Gly	Pro	Val	Glu	Ile	Gly	Leu	305	310	315	320
Pro	Cys	Ser	Ile	Lys	Asn	Glu	Ala	Arg	Pro	Pro	Cys	Leu	Pro	Thr	Pro	325	330	335	
Gly	Lys	Arg	Glu	Pro	Gln	Gly	Ile	Ser	Trp	Glu	Ser	Pro	Leu	Asp	Glu	340	345	350	
Val	Asp	Lys	Met	Cys	His	Leu	Pro	Glu	Pro	Glu	Leu	Asn	Lys	Glu	Arg	355	360	365	

Pro Ser Leu Gln Ile Lys Leu Lys Ile Glu Asp Phe Ile Leu His Lys
 370 375 380
 Met Leu Gly Lys Gly Ser Phe Gly Lys Val Phe Leu Ala Glu Phe Lys
 385 390 395 400
 Lys Thr Asn Gln Phe Phe Ala Ile Arg Ala Leu Lys Lys Asp Val Val
 405 410 415
 Leu Met Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val Leu
 420 425 430
 Ser Leu Ala Trp Glu His Pro Phe Leu Thr His Met Phe Cys Thr Phe
 435 440 445
 Gln Thr Lys Glu Asn Leu Phe Phe Val Met Glu Tyr Leu Asn Gly Gly
 450 455 460
 Asp Leu Met Tyr His Ile Gln Ser Cys His Lys Phe Asp Leu Ser Arg
 465 470 475 480
 Ala Thr Phe Tyr Ala Ala Glu Ile Ile Leu Gly Leu Gln Phe Leu His
 485 490 495
 Ser Lys Gly Ile Val Tyr Arg Asp Leu Lys Leu Asp Asn Ile Leu Leu
 500 505 510
 Asp Lys Asp Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys Glu
 515 520 525
 Asn Met Leu Gly Asp Ala Lys Thr Asn Thr Phe Cys Gly Thr Pro Asp
 530 535 540
 Tyr Ile Ala Pro Glu Ile Leu Leu Gly Gln Lys Tyr Asn His Ser Val
 545 550 555 560
 Asp Trp Trp Ser Phe Gly Val Leu Leu Tyr Glu Met Leu Ile Gly Gln
 565 570 575
 Ser Pro Phe His Gly Gln Asp Glu Glu Glu Leu Phe His Ser Ile Arg
 580 585 590
 Met Asp Asn Pro Phe Tyr Pro Arg Trp Leu Glu Lys Glu Ala Lys Asp
 595 600 605
 Leu Leu Val Lys Leu Phe Val Arg Glu Pro Glu Lys Arg Leu Gly Val
 610 615 620
 Arg Gly Asp Ile Arg Gln His Pro Leu Phe Arg Glu Ile Asn Trp Glu
 625 630 635 640
 Glu Leu Glu Arg Lys Glu Ile Asp Pro Pro Phe Arg Pro Lys Val Lys
 645 650 655
 Ser Pro Phe Asp Cys Ser Asn Phe Asp Lys Glu Phe Leu Asn Glu Lys
 660 665 670

Pro Arg Leu Ser Phe Ala Asp Arg Ala Leu Ile Asn Ser Met Asp Gln
 675 680 685

Asn Met Phe Arg Asn Phe Ser Phe Met Asn Pro Gly Met Glu Arg Leu
 690 695 700

Ile Ser
 705

<210> 11

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 enhancer oligonucleotide

<400> 11

tggggacttt ccgc